

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Forschungszentrum Juelich GmbH
- (B) ADDRESS: Postfach 1913
- (C) CITY: Juelich
- (E) COUNTRY: GERMANY
- (F) ZIP CODE: 52425

(ii) TITLE OF INVENTION: METHOD FOR MICROBIAL PRODUCTION OF AMINO ACIDS OF THE ASPARTATE AND/OR GLUTAMATE FAMILY

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3728 Base Pairs
- (B) Type: Nucleotide
- (C) Strandedness: Single strand
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: Genomic DNA

(xi) SEQ ID NO: 1:

CGCAACCGTG CTTGAAGTCG TGCAGGTCAG GGGAGTGTTG CCCGAAAACA TTGAGAGGAA	60
AACAAAAACC GATGTTTGAT TGGGGGAATC GGGGGTTACG ATACTAGGAC GCAGTGACTG	120
CTATCACCTT TGGCGGTCTC TTGTTGAAAG GAATAATTAC TCTAGTGTCG ACTCACACAT	180
CTTCAACGCT TCCAGCATTC AAAAAGATCT TGGTAGCAAA CCGCGGCGAA ATCGCGGTCC	240
GTGCTTTCCG TGCAGCACTC GAAACCGGTG CAGCCACGGT AGCTATTTAC CCCCCTGAAG	300
ATCGGGGATC ATTCCACCGC TCTTTTGCTT CTGAAGCTGT CCGCATTTGGT ACCGAAGGCT	360
CACCAGTCAA GCGGTACCTG GACATCGATG AAATTATCGG TGCAGCTAAA AAAGTTAAAG	420
CAGATGCCAT TTACCCGGGA TACGGCTTCC TGTCTGAAAA TGCCCAGCTT GCCCGCGAGT	480

GTGCGGAAAA	CGGCATTACT	TTTATTGGCC	CAACCCCAGA	GGTTCTTGAT	CTCACCGGTG	540
ATAAGTCTCG	CGCGGTAACC	GCCGCGAAGA	AGGCTGGTCT	GCCAGTTTTG	GCGGAATCCA	600
CCCCGAGCAA	AAACATCGAT	GAGATCGTTA	AAAGCGCTGA	AGGCCAGACT	TACCCCATCT	660
TTGTGAAGGC	AGTTGCCGGT	GGTGGCGGAC	GCGGTATGCG	TTTTGTTGCT	TCACCTGATG	720
AGCTTCGCAA	ATTAGCAACA	GAAGCATCTC	GTGAAGCTGA	AGCGGCTTTC	GGCGATGGCG	780
CGGTATATGT	CGAACGTGCT	GTGATTAACC	CTCAGCATAT	TGAAGTGCAG	ATCCTTGGCG	840
ATCACACTGG	AGAAGTTGTA	CACCTTTATG	AACGTGACTG	CTCACTGCAG	CGTCGTCACC	900
AAAAAGTTGT	CGAAATTGCG	CCAGCACAGC	ATTTGGATCC	AGAACTGCGT	GATCGCATTT	960
GTGCGGATGC	AGTAAAGTTC	TGCCGCTCCA	TTGGTTACCA	GGGCGCGGGA	ACCGTGGAAT	1020
TCTTGGTCGA	TGAAAAGGGC	AACCACGTCT	TCATCGAAAT	GAACCCACGT	ATCCAGGTTG	1080
AGCACACCGT	GACTGAAGAA	GTCACCGAGG	TGGACCTGGT	GAAGGCGCAG	ATGCGCTTGG	1140
CTGCTGGTGC	AACCTTGAAG	GAATTGGGTC	TGA CC CAAGA	TAAGATCAAG	ACCCACGGTG	1200
CAGCACTGCA	GTGCCGCATC	ACCACGGAAG	ATCCAAACAA	CGGCTTCCGC	CCAGATACCG	1260
GAACTATCAC	CGCGTACCGC	TCACCAGGCG	GAGCTGGCGT	TCGTCTTGAC	GGTGCAGCTC	1320
AGCTCGGTGG	CGAAATCACC	GCACACTTTG	ACTCCATGCT	GGTGAAAATG	ACCTGCCGTG	1380
GTTCCGACTT	TGAAACTGCT	GTTGCTCGTG	CACAGCGCGC	GTTGGCTGAG	TTCACCGTGT	1440
CTGGTGTGTC	AACCAACATT	GGTTTCTTGC	GTGCGTTGCT	GCGGGAAGAG	GACTTCACTT	1500
CCAAGCGCAT	CGCCACCGGA	TTCATTGCCG	ATCACCCGCA	CCTCCTTCAG	GCTCCACCTG	1560
CTGATGATGA	GCAGGGACGC	ATCCTGGATT	ACTTGGCAGA	TGTCACCGTG	AACAAGCCTC	1620
ATGGTGTGCG	TCCAAAGGAT	GTTGCAGCTC	CTATCGATAA	GCTGCCTAAC	ATCAAGGATC	1680
TGCCACTGCC	ACGCGGTTCC	CGTGACCGCC	TGAAGCAGCT	TGGCCCAGCC	GCGTTTGCTC	1740
GTGATCTCCG	TGAGCAGGAC	GCACTGGCAG	TTACTGATAC	CACCTTCCGC	GATGCACACC	1800
AGTCTTTGCT	TGCGACCCGA	GTCCGCTCAT	TCGCACTGAA	GCCTGCGGCA	GAGGCCGTCTG	1860
CAAAGCTGAC	TCCTGAGCTT	TTGTCCGTGG	AGGCCTGGGG	CGGCGCGACC	TACGATGTGG	1920
CGATGCGTTT	CCTCTTTGAG	GATCCGTGGG	ACAGGCTCGA	CGAGCTGCGC	GAGGCGATGC	1980
CGAATGTAAA	CATTCAGATG	CTGCTTCGCG	GCCGCAACAC	CGTGGGATAC	ACCCCGTACC	2040
CAGACTCCGT	CTGCCGCGCG	TTTGTTAAGG	AAGCTGCCAG	CTCCGGCGTG	GACATCTTCC	2100

GCATCTTCGA	CGCGCTTAAC	GACGTCTCCC	AGATGCGTCC	AGCAATCGAC	GCAGTCCTGG	2160
AGACCAACAC	CGCGGTAGCC	GAGGTGGCTA	TGGCTTATTC	TGGTGATCTC	TCTGATCCAA	2220
ATGAAAAGCT	CTACACCCTG	GATTACTACC	TAAAGATGGC	AGAGGAGATC	GTCAAGTCTG	2280
GCGCTCACAT	CTTGGCCATT	AAGGATATGG	CTGGTCTGCT	TCGCCCAGCT	GCGGTAACCA	2340
AGCTGGTCAC	CGCACTGCGC	CGTGAATTCG	ATCTGCCAGT	GCACGTGCAC	ACCCACGACA	2400
CTGCGGGTGG	CCAGCTGGCA	ACCTACTTTG	CTGCAGCTCA	AGCTGGTGCA	GATGCTGTTG	2460
ACGGTGCTTC	CGCACCCTG	TCTGGCACCA	CCTCCCAGCC	ATCCCTGTCT	GCCATTGTTG	2520
CTGCATTTCG	GCACACCCGT	CGCGATACCG	GTTTGAGCCT	CGAGGCTGTT	TCTGACCTCG	2580
AGCCGTA CTG	GGAAGCAGTG	CGCGGACTGT	ACCTGCCATT	TGAGTCTGGA	ACCCCAGGCC	2640
CAACCGGTCTG	CGTCTACCGC	CACGAAATCC	CAGGCGGACA	GTTGTCCAAC	CTGCGTGCAC	2700
AGGCCACCGC	ACTGGGCCTT	GCGGATCGTT	TCGAACTCAT	CGAAGACAAC	TACGCAGCCG	2760
TTAATGAGAT	GCTGGGACGC	CCAACCAAGG	TSACCCCATC	CTCCAAGGTT	GTTGGCGACC	2820
TCGCACTCCA	CCTCGTTGGT	GCGGGTGTGG	ATCCAGCAGA	CTTTGCTGCC	GATCCACAAA	2880
AGTACGACAT	CCCAGACTCT	GTCATCGCGT	TCCTGCGCGG	CGAGCTTGGT	AACCCTCCAG	2940
GTGGCTGGCC	AGAGCCACTG	CGCACCCGCG	CACTGGAAGG	CCGCTCCGAA	GGCAAGGCAC	3000
CTCTGACGGA	AGTTCCTGAG	GAAGAGCAGG	CGCACCTCGA	CGCTGATGAT	TCCAAGGAAC	3060
GTCGCAATAG	CCTCAACCGC	CTGCTGTTCC	CGAAGCCAAC	CGAAGAGTTC	CTCGAGCACC	3120
GTCGCCGCTT	CGGCAACACC	TCTGCGCTGG	ATGATCGTGA	ATTCTTCTAC	GGCCTGGTCG	3180
AAGGCCGCGA	GACTTTGATC	CGCCTGCCAG	ATGTGCGCAC	CCCACTGCTT	GTTGCGCTGG	3240
ATGCGATCTC	TGAGCCAGAC	GATAAGGGTA	TGCGCAATGT	TGTGGCCAAC	GTCAACGGCC	3300
AGATCCGCCC	AATGCGTGTG	CGTGACCGCT	CCGTTGAGTC	TGTCACCGCA	ACCGCAGAAA	3360
AGGCAGATTC	CTCCAACAAG	GGCCATGTTG	CTGCACCATT	CGCTGGTGTT	GTCACCGTGA	3420
CTGTTGCTGA	AGGTGATGAG	GTCAAGGCTG	GAGATGCAGT	CGCAATCATC	GAGGCTATGA	3480
AGATGGAAGC	AACAATCACT	GCTTCTGTTG	ACGGCAAAAT	CGATCGCGTT	GTGGTTCCTG	3540
CTGCAACGAA	GGTGGAAGGT	GGCGACTTGA	TCGTCGTCGT	TTCTTAAACC	TTTCTGTAAA	3600
AAGCCCCGCG	TCTTCCTCAT	GGAGGAGGCG	GGGCTTTTTG	GGCCAAGATG	GGAGATGGGT	3660
GAGTTGGATT	TGGTCTGATT	CGACACTTTT	AAGGGCAGAG	ATTTGAAGAT	GGAGACCAAG	3720

(2) SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Single Strand
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: Protein

(xi) SEQ ID NO: 2:

Met Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu
1 5 10 15

Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu
20 25 30

Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
35 40 45

Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
50 55 60

Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala
65 70 75 80

Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu
85 90 95

Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
100 105 110

Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
115 120 125

Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
130 135 140

Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
145 150 155 160

Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
165 170 175

Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr
180 185 190

Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr

195				200				205							
Val	Glu	Arg	Ala	Val	Ile	Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu
210						215					220				
Gly	Asp	His	Thr	Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser
225				230						235					240
Leu	Gln	Arg	Arg	His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His
				245						250				255	
Leu	Asp	Pro	Glu	Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe
			260					265					270		
Cys	Arg	Ser	Ile	Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val
		275						280					285		
Asp	Glu	Lys	Gly	Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln
	290					295					300				
Val	Glu	His	Thr	Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys
305					310					315					320
Ala	Gln	Met	Arg	Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu
				325					330					335	
Thr	Gln	Asp	Lys	Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile
			340						345				350		
Thr	Thr	Glu	Asp	Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile
		355						360					365		
Thr	Ala	Tyr	Arg	Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala
	370					375					380				
Ala	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val
385					390					395					400
Lys	Met	Thr	Cys	Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala
				405					410					415	
Gln	Arg	Ala	Leu	Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile
			420						425					430	
Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys	Arg
		435					440					445			
Ile	Ala	Thr	Gly	Phe	Ile	Ala	Asp	His	Pro	His	Leu	Leu	Gln	Ala	Pro
	450					455					460				
Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp	Val
465					470					475					480
Thr	Val	Asn	Lys	Pro	His	Gly	Val	Arg	Pro	Lys	Asp	Val	Ala	Ala	Pro

485										490					495				
Ile	Asp	Lys	Leu	Pro	Asn	Ile	Lys	Asp	Leu	Pro	Leu	Pro	Arg	Gly	Ser				
			500					505					510						
Arg	Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Ala	Ala	Phe	Ala	Arg	Asp	Leu				
		515					520					525							
Arg	Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr	Phe	Arg	Asp	Ala				
	530					535					540								
His	Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe	Ala	Leu	Lys	Pro				
545					550					555					560				
Ala	Ala	Glu	Ala	Val	Ala	Lys	Lys	Thr	Pro	Glu	Leu	Leu	Ser	Val	Glu				
				565					570					575					
Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	Phe	Leu	Phe	Glu				
			580					585					590						
Asp	Pro	Trp	Asp	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	Met	Pro	Asn	Val				
		595					600					605							
Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr	Pro				
	610					615					620								
Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Lys	Glu	Ala	Ala	Ser	Ser				
625					630					635					640				
Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn	Asp	Val	Ser	Gln				
				645					650					655					
Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Asn	Thr	Ala	Val	Ala				
			660					665					670						
Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asp	Pro	Asn	Glu	Lys				
		675					680					685							
Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Lys	Met	Ala	Glu	Glu	Ile	Val	Lys				
	690					695					700								
Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	Lys	Asp	Met	Xaa	Gly	Leu	Leu	Arg				
705					710					715					720				
Pro	Ala	Ala	Val	Thr	Lys	Leu	Val	Thr	Ala	Leu	Arg	Arg	Glu	Phe	Asp				
				725					730					735					
Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	Ala				
			740					745					750						
Thr	Tyr	Phe	Ala	Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly	Ala				
		755					760					765							
Ser	Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser	Leu	Ser	Ala	Ile				

770						775						780					
Val	Ala	Ala	Phe	Ala	His	Thr	Arg	Arg	Asp	Thr	Gly	Leu	Ser	Leu	Glu		
785					790					795					800		
Ala	Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val	Arg	Gly	Leu	Tyr		
				805					810					815			
Leu	Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly	Arg	Val	Tyr	Arg		
			820					825					830				
His	Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg	Ala	Gln	Ala	Thr		
		835					840					845					
Ala	Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu	Asp	Asn	Tyr	Ala		
	850					855					860						
Ala	Val	Asn	Glu	Met	Leu	Gly	Arg	Pro	Thr	Lys	Val	Thr	Pro	Ser	Ser		
865					870					875					880		
Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	Asp		
				885					890					895			
Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	Ser		
			900				905						910				
Val	Ile	Ala	Phe	Leu	Arg	Gly	Glu	Leu	Gly	Asn	Pro	Pro	Gly	Gly	Trp		
		915					920						925				
Pro	Glu	Pro	Leu	Arg	Thr	Arg	Ala	Leu	Glu	Gly	Arg	Ser	Glu	Gly	Lys		
	930					935						940					
Ala	Pro	Leu	Thr	Glu	Val	Pro	Glu	Glu	Glu	Gln	Ala	His	Leu	Asp	Ala		
945					950					955					960		
Asp	Asp	Ser	Lys	Glu	Arg	Arg	Asn	Ser	Leu	Asn	Arg	Leu	Leu	Phe	Pro		
				965					970					975			
Lys	Pro	Thr	Glu	Glu	Phe	Leu	Glu	His	Arg	Arg	Arg	Phe	Gly	Asn	Thr		
			980					985					990				
Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe	Tyr	Gly	Leu	Val	Glu	Gly	Arg		
		995					1000					1005					
Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val	Arg	Thr	Pro	Leu	Leu	Val	Arg		
	1010					1015						1020					
Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp	Lys	Gly	Met	Arg	Asn	Val	Val		
1025					1030					1035					1040		
Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro	Met	Arg	Val	Arg	Asp	Arg	Ser		
				1045					1050					1055			
Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu	Lys	Ala	Asp	Ser	Ser	Asn	Lys		

1060

1065

1070

Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala
1075 1080 1085

Glu Gly Asp Glu Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala
1090 1095 1100

Met Lys Met Glu Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp
1105 1110 1115 1120

Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile
1125 1130 1135

Val Val Val Ser
1140

Bl
Cmt